



# Operational Dynamics and Challenges using DSI across Biodiversity Frameworks

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*10th Governing body of ITPGRFA - Side event  
“Building a harmonized system to increase fair and equitable benefit  
sharing from the use of Digital Sequence Information.”*

# CGIAR Genebanks



International Musa germplasm Transit Centre (ITC), Belgium

# Bananas (Musa spp), a staple food crop under multiple stresses



Viral, bacterial and fungal diseases

# Virus indexing

RESEARCH



## Validation of High-Throughput Sequencing as Virus Indexing Test for *Musa* Germplasm: Performance Criteria Evaluation and Contamination Monitoring Using an Alien Control

Wei Rong, Johan Rollin, Marwa Hanafi, Nicolas Roux, and Sebastien Massart ✉



Sebastien Massart,  
Belgium



Nine virus species  
including  
Banana Bunchy Top Virus (BBTV)  
Banana Streak Virus (BSV)



*Genebank material distribution*

# Fusarium wilt (TR4)

## THE OTHER PANDEMIC

Panama wilt infection has spread aggressively to commercial banana plantations in 18 countries since it was first detected in 1970



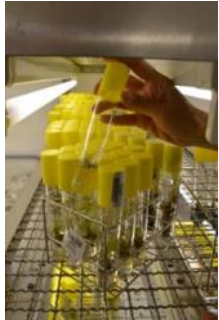
00 The year Panama wilt first made an appearance in the country

Source: Food and Agriculture Organization

# Genetic mechanisms of disease resistance



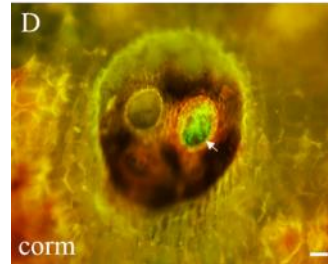
Sijun Zheng,  
China



**Resistant**  
Wild banana  
(Genebank SMTA)

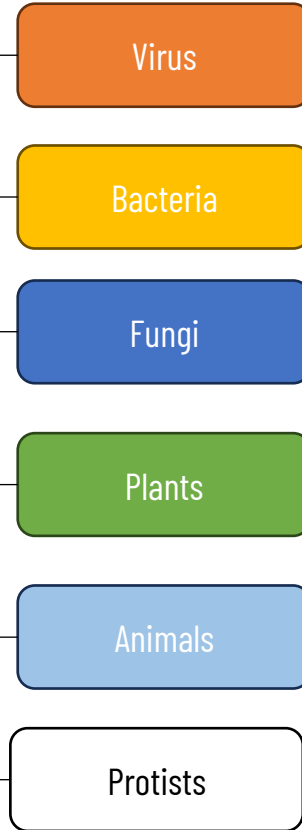
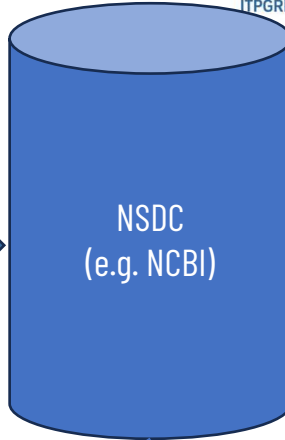


**Susceptible**  
Cavendish 'Brazilian'  
(China University)



**Fusarium TR4**  
pathogenic strain  
(Genetic engineered)

# Bioinformatics analyses



Candidate genes



Alberto Cenci,  
France



# First Report of *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 Causing Fusarium Wilt in Cavendish Bananas in Peru

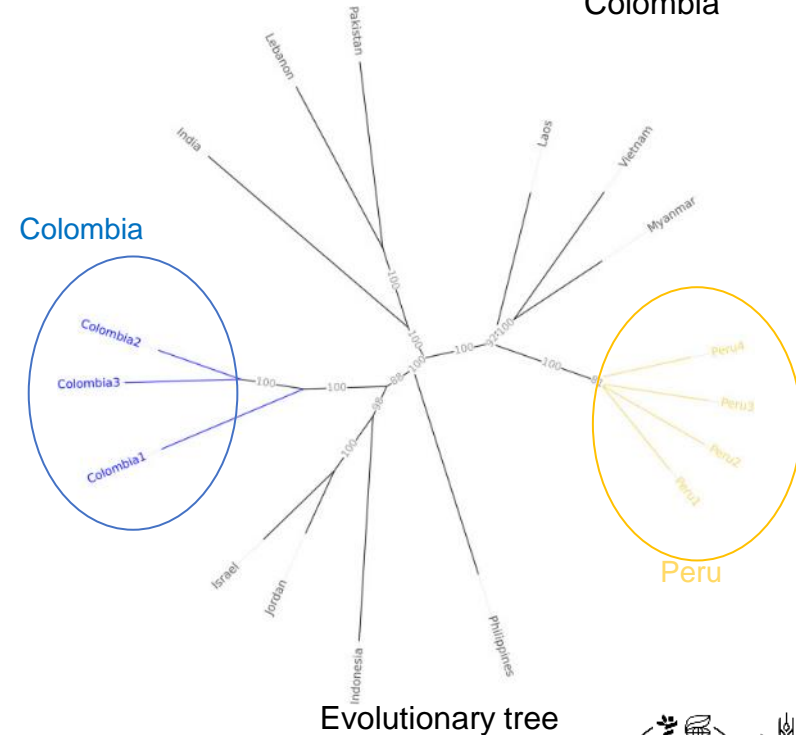
R. Acuña, M. Rouard, A. M. Leiva, C. Marques, J. A. Olortegui, C. Ureta, R. M. Cabrera-Pintado, J. C. Rojas, D. Lopez-Alvarez, A. Cenci, W. J. Cuellar, and M. Dita ✉

Affiliations ▾

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Miguel Dita,  
Colombia





# Understanding virus diversity, distribution and their impacts on crops production



Jan Kreuze,  
Peru



## Pan-African Sweet Potato Virome

Home Sampling Data Participants Publication Link

**Determining the Pan-African sweetpotato virome: understanding virus diversity, distribution and evolution and their impacts on sweetpotato production in Africa**

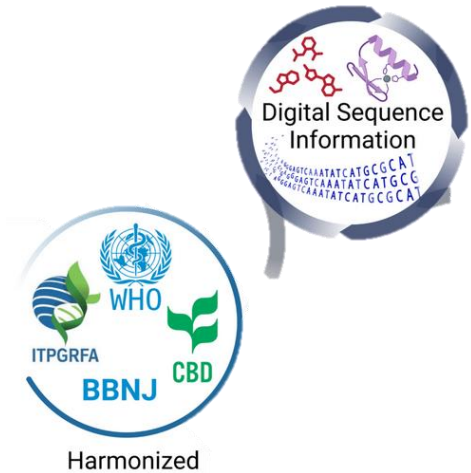
Sweetpotato is among the most important food crops in the world and an extremely important food crop for subsistence farmers in sub-Saharan Africa (SSA). It is grown throughout the African continent and currently around 34.5% of global sweetpotato area is in Africa. One major limitation in sweetpotato production is cultivar decline, mostly due to the cumulative effect of virus infection on this vegetatively propagated crop. Thus, viral diseases are considered a major limiting factor in sweetpotato production worldwide, particularly in SSA. We used a novel approach, deep sequencing of small RNAs from field-grown sweetpotato samples collected throughout Africa, to systematically and efficiently identify known and novel virus genome sequences. A total of around 1200 gcc-referenced field-grown samples of sweetpotato have been collected from more than ten countries in Africa. Small RNA populations of these samples have been prepared and sequenced using high throughput next-generation sequencing technology, and then mapped and assembled to identify known and novel sweetpotato viruses.

Food security remains a huge challenge for millions of Africans, particularly for those in sub-Saharan regions, who depend on agriculture for their subsistence. Emerging and reemerging pathogens, including many viruses, continue to cause devastating losses of food production in Africa. Current knowledge of crop viruses in Africa is limited and sporadic at best. Novel virus genome identification technology through deep sequencing of small RNA population is potentially applicable to continental surveys as its efficiency in virus identification has been proven with both greenhouse and field grown samples. This technology can then be applied to systematically determine the total virus genome sequences (virome) on a number of other major crop plants in Africa. Public availability of such information will provide the scientific community and government unprecedented possibilities to understand crop virus distribution in Africa, guide phytosanitary requirements, predict risks of future epidemics, and suggest regional disease management strategies.

Sweet potato production in Africa

# Take home messages

- Data remain accessible and continue to provide value beyond the project cycle
- Most scientists are NOT experts in multiple policy frameworks
- Scientists need practical and sync frameworks to operate using DSI (e.g. ITPGRFA annex 1 crops with pathogens)
- Access & use of DSI and benefit sharing from DSI should be delinked





Thank you for  
your attention

